

50 Years of Neutron Backscattering Spectroscopy



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Protein diffusion in crowded solutions

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New backscattering spectrometers give an unprecedented access to the hierarchical dynamics of proteins in solution [1-3]. The new tools can for instance be used to explore the biologically important impact of macromolecular crowding on the global and internal dynamics of proteins in an aqueous environment. Moreover, the effect of salt-induced charges on the protein diffusion becomes accessible [4]. The global translational center-of-mass motion on the nanosecond time scale and its dependence on the protein volume fraction can be interpreted in terms of the short-time diffusion of colloidal hard spheres [1]. Recent experiments additionally indicate a qualitative agreement of the internal protein motions, consisting of backbone and side-chain motions, with intuitive expectations in a wide temperature range from the native to the denatured state [1-2]. Recent systematic measurements as a function of the salt-induced charges show a universal scaling behavior of the protein diffusion depending on the salt concentration and crowding [4]. [1] M.Grimaldo et al., JPCB 118, 7203 (2014); [2] M.Grimaldo et al., PCCP 17, 4645 (2015); [3] M.Grimaldo et al., EPJ Web of Conf. 83, 02005 (2015); [4] M.Grimaldo et al., JPCL 6, 2577 (2015).

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